OIPE

ENTERED

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/846,589A

DATE: 03/11/2002
TIME: 09:44:16

Input Set : **A:\BB-1191 Seq List.txt**
Output Set: **N:\CRF3\03112002\I846589A.raw**

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    3  <110>  APPLICANT: Famodu, Layo O.
    4          Orozco, Buddy
    5          Rafalski, Antoni
    7  <120>  TITLE OF INVENTION: Plant Aminoacyl-tRNA Synthetase
    9  <130>  FILE REFERENCE: BB-1191
C-->  11  <140>  CURRENT APPLICATION NUMBER: US/09/846,589A
C-->  12  <141>  CURRENT FILING DATE: 2002-01-22
   14  <150>  PRIOR APPLICATION NUMBER: 60/092,866
W-->  15  <151>  PRIOR FILING DATE: July 15, 1998
   17  <160>  NUMBER OF SEQ ID NOS: 29
   19  <170>  SOFTWARE: Microsoft Office 97
   21  <210>  SEQ ID NO: 1
   22  <211>  LENGTH: 1948
   23  <212>  TYPE: DNA
   24  <213>  ORGANISM: Zea mays
   26  <400>  SEQUENCE: 1
   27  cgcacgatag ccgccgccgt cgaccagagc actcccccgt cgtcgccacg atgtcgtctg    60
   28  agcctccacc cgcctcctct gccgccgccg gagaggaact cgctgctgac ctttccgccg   120
   29  ctaccctcag caagaagcag cagaagaagg acgcgaggaa ggcggagaag gcagagcagc   180
   30  gccagcgtca gcagcagcag cagcagcagc cggcggacgc cgaggacccg ttcgcggcca   240
   31  actacggcga ggtccccgtc gaggagatcc agtcaaaggc catctccggc cgctcgtggt   300
   32  cccatgtcgg cgacctcgac gactccgctg cgggccgctc cgtgcttatc cgcggagccg   360
   33  cgcaggccat ccgtccggtc agcaagaaga tggctttcgt cgtgctgcgc cagagtatga   420
   34  gcaccgtgca gtgcgtgctc gtcgccagcg ccgacgccgg cgtcagcacg cagatggtgc   480
   35  gcttcgccac cgccctcagc aaggagtcca tcgtcgacgt tgagggcgtc gtctccctcc   540
   36  caaaggagcc cctcaaggcc accacacagc aggttgagat ccaagtgagg aagatctatt   600
   37  gcatcaatag ggctattccg acccttccaa ttaaccttga agatgcggct cggagtgagg   660
   38  cagattttga gaaggctgaa ttggctggag aaaagcttgt tcgcgttggc caagataccc   720
   39  gcttgaacta cagagctatt gatctacgaa caccctcgaa tcaagccata ttccggatcc   780
   40  agtgtcaagt tgaaaacaaa tttagagatt ttttgttgtc gaagaacttt gtcgggatcc   840
   41  acaccccaaa attgatttct ggatctagtg aagggggtgc ggctgtattc aagcttctgt   900
   42  acaatggtca acctgcttgt ttggcacaat cccctcagtt atacaagcaa atggctatct   960
   43  ctggtggttt tgagcgagta tttgaggtcg ccctgtgtt tagagcagaa aattcaaaca  1020
   44  cacacaggca tctatgtgag ttcgttggtc ttgatgctga atggagatt aaggagcatt  1080
   45  attttgaggt ctgtgacatt atagatggct tattcgtatc aatatttaaa cacttgtctg  1140
   46  aaaactgcaa gaaagaactc gaatcaataa acaggcagta tccatttgaa cctctgaagt  1200
   47  atctagacaa aacctttaag ctcacttatg aagaaggaat tcaaatgttg aaggaagccg  1260
   48  gaacagaaat cgagcctatg ggtgacctca ataccgaagc tgagaaaaaa cttggtcggc  1320
   49  ttgtcaggga aaagtatgac acagattttt tcatcctgta tcggtatcct ttggctgtac  1380
   50  gtccgttcta caccatgcct tgttatgaca acccagcgta caccaattct tttgatgtct  1440
   51  tcattcgagg cgaggagata atatctggag cacaaaggat acacactcct gagctgctgg  1500
   52  ccaagcgcgc gacagagtgt ggaatcgacg tgagcactat ctcggcctac attgaatcct  1560
   53  tcagctatgg cgtgccgcca cacggcggtt cggggtgggg tttggagagg gtggtgatgc  1620
```

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54 tgttctgtgc cctgaacaac atcaggaaga cctccctgtt cccgcgcgac ccgcagaggc 1680
55 tcgtgccgta agtttctgat tccaagcctg agtcttcgag tggtctacgg agcagatccg 1740
56 atgttgttac catcagagtt gacttgcaat cttagctcct gaacctggcg gttaccgtgg 1800
57 atcagagttc ctgttgaatt tcacaaaagc ctacttgttc ctaatagatt gctgcaacca 1860
58 acaatattac gaccctttcg ggcttttctt cccgcctcac gtgttattct ggtctatact 1920
59 tgtttttaag tgcaagtatt gctcagtt                                    1948
61 <210> SEQ ID NO: 2
62 <211> LENGTH: 546
63 <212> TYPE: PRT
64 <213> ORGANISM: Zea mays
66 <400> SEQUENCE: 2
67 Met Ser Ser Glu Pro Pro Pro Ala Ser Ser Ala Ala Ala Gly Glu Glu
68  1               5                  10                  15
70 Leu Ala Ala Asp Leu Ser Ala Ala Thr Leu Ser Lys Lys Gln Gln Lys
71              20                  25                  30
73 Lys Asp Ala Arg Lys Ala Glu Lys Ala Glu Gln Arg Gln Arg Gln Gln
74          35                  40                  45
76 Gln Gln Gln Gln Gln Pro Ala Asp Ala Glu Asp Pro Phe Ala Ala Asn
77      50                  55                  60
79 Tyr Gly Glu Val Pro Val Glu Glu Ile Gln Ser Lys Ala Ile Ser Gly
80 65                  70                  75                  80
82 Arg Ser Trp Ser His Val Gly Asp Leu Asp Asp Ser Ala Ala Gly Arg
83              85                  90                  95
85 Ser Val Leu Ile Arg Gly Ala Ala Gln Ala Ile Arg Pro Val Ser Lys
86              100                 105                 110
88 Lys Met Ala Phe Val Val Leu Arg Gln Ser Met Ser Thr Val Gln Cys
89          115                 120                 125
91 Val Leu Val Ala Ser Ala Asp Ala Gly Val Ser Thr Gln Met Val Arg
92      130                 135                 140
94 Phe Ala Thr Ala Leu Ser Lys Glu Ser Ile Val Asp Val Glu Gly Val
95 145                 150                 155                 160
97 Val Ser Leu Pro Lys Glu Pro Leu Lys Ala Thr Thr Gln Gln Val Glu
98              165                 170                 175
100 Ile Gln Val Arg Lys Ile Tyr Cys Ile Asn Arg Ala Ile Pro Thr Leu
101             180                 185                 190
103 Pro Ile Asn Leu Glu Asp Ala Ala Arg Ser Glu Ala Asp Phe Glu Lys
104         195                 200                 205
106 Ala Glu Leu Ala Gly Glu Lys Leu Val Arg Val Gly Gln Asp Thr Arg
107     210                 215                 220
109 Leu Asn Tyr Arg Ala Ile Asp Leu Arg Thr Pro Ser Asn Gln Ala Ile
110 225                 230                 235                 240
112 Phe Arg Ile Gln Cys Gln Val Glu Asn Lys Phe Arg Asp Phe Leu Leu
113             245                 250                 255
115 Ser Lys Asn Phe Val Gly Ile His Thr Pro Lys Leu Ile Ser Gly Ser
116             260                 265                 270
118 Ser Glu Gly Gly Ala Ala Val Phe Lys Leu Leu Tyr Asn Gly Gln Pro
119         275                 280                 285
121 Ala Cys Leu Ala Gln Ser Pro Gln Leu Tyr Lys Gln Met Ala Ile Ser
122     290                 295                 300
```

```
124 Gly Gly Phe Glu Arg Val Phe Glu Val Gly Pro Val Phe Arg Ala Glu
125 305             310             315             320
127 Asn Ser Asn Thr His Arg His Leu Cys Glu Phe Val Gly Leu Asp Ala
128             325             330             335
130 Glu Met Glu Ile Lys Glu His Tyr Phe Glu Val Cys Asp Ile Ile Asp
131             340             345             350
133 Gly Leu Phe Val Ser Ile Phe Lys His Leu Ser Glu Asn Cys Lys Lys
134         355             360             365
136 Glu Leu Glu Ser Ile Asn Arg Gln Tyr Pro Phe Glu Pro Leu Lys Tyr
137     370             375             380
139 Leu Asp Lys Thr Phe Lys Leu Thr Tyr Glu Glu Gly Ile Gln Met Leu
140 385             390             395             400
142 Lys Glu Ala Gly Thr Glu Ile Glu Pro Met Gly Asp Leu Asn Thr Glu
143             405             410             415
145 Ala Glu Lys Lys Leu Gly Arg Leu Val Arg Glu Lys Tyr Asp Thr Asp
146         420             425             430
148 Phe Phe Ile Leu Tyr Arg Tyr Pro Leu Ala Val Arg Pro Phe Tyr Thr
149         435             440             445
151 Met Pro Cys Tyr Asp Asn Pro Ala Tyr Thr Asn Ser Phe Asp Val Phe
152     450             455             460
154 Ile Arg Gly Glu Glu Ile Ile Ser Gly Ala Gln Arg Ile His Thr Pro
155 465             470             475             480
157 Glu Leu Leu Ala Lys Arg Ala Thr Glu Cys Gly Ile Asp Val Ser Thr
158             485             490             495
160 Ile Ser Ala Tyr Ile Glu Ser Phe Ser Tyr Gly Val Pro Pro His Gly
161         500             505             510
163 Gly Phe Gly Val Gly Leu Glu Arg Val Val Met Leu Phe Cys Ala Leu
164         515             520             525
166 Asn Asn Ile Arg Lys Thr Ser Leu Phe Pro Arg Asp Pro Gln Arg Leu
167     530             535             540
169 Val Pro
170 545
172 <210> SEQ ID NO: 3
173 <211> LENGTH: 730
174 <212> TYPE: DNA
175 <213> ORGANISM: Oryza sativa
177 <400> SEQUENCE: 3
178 gcacgagctt acacggcacg agcttacagg aattcaaatg ctgaaggaag ctggaacaga   60
179 aatcgaaccc atgggtgacc tcaacactga agctgagaaa aaactaggcc ggcttgttaa  120
180 ggagaagtat ggaacagaat ttttcatcct ctatcggtat cctttggctg tgcgtccctt  180
181 ctacaccatg ccttgttatg acaacccagc ttacagtaac tcttttgatg tctttattcg  240
182 aggagaggaa ataatatctg gagcacaaag aatacattta ccagagctat tgacgaaacg  300
183 tgcaacagag tgtggaattg atgcgagtac tatttcatca tatatcgaat cgttcagcta  360
184 tggtgcacct cctcatggtg gttttggtgt cggcctggag agggtggtaa tgctgttctg  420
185 cgccctaaac aacatcagga agacatcact tttccctcgc gatccacaaa ggctggtgcc  480
186 ataatttgct tttttttccca agagcaaggt ttggactcag tacggactgg gcagttttcc  540
187 tcggctggtt tttttacctg gacattattt tcgtatttat taatgtgctg tactgcaaaa  600
188 gctgctcctt ccacaacat ttggaatagt tgccgataca tttggaatag ggctcaacgt  660
189 tggcgttgtg atttcgttga tgatcccgct attcgtaaca aaaaaaaaa aaaaaaaaaa  720
```

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Input Set : A:\BB-1191 Seq List.txt
Output Set: N:\CRF3\03112002\I846589A.raw

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190 aaaaaaaaaa                                                          730
192 <210> SEQ ID NO: 4
193 <211> LENGTH: 148
194 <212> TYPE: PRT
195 <213> ORGANISM: Oryza sativa
197 <400> SEQUENCE: 4
198 Met Leu Lys Glu Ala Gly Thr Glu Ile Glu Pro Met Gly Asp Leu Asn
199   1               5                  10              .    15
201 Thr Glu Ala Glu Lys Lys Leu Gly Arg Leu Val Lys Glu Lys Tyr Gly
202             20                  25                  30
204 Thr Glu Phe Phe Ile Leu Tyr Arg Tyr Pro Leu Ala Val Arg Pro Phe
205         35                  40                  45
207 Tyr Thr Met Pro Cys Tyr Asp Asn Pro Ala Tyr Ser Asn Ser Phe Asp
208     50                  55                  60
210 Val Phe Ile Arg Gly Glu Glu Ile Ile Ser Gly Ala Gln Arg Ile His
211 65                  70                  75                  80
213 Leu Pro Glu Leu Leu Thr Lys Arg Ala Thr Glu Cys Gly Ile Asp Ala
214                 85                  90                  95
216 Ser Thr Ile Ser Ser Tyr Ile Glu Ser Phe Ser Tyr Gly Ala Pro Pro
217             100                 105                 110
219 His Gly Gly Phe Gly Val Gly Leu Glu Arg Val Val Met Leu Phe Cys
220         115                 120                 125
222 Ala Leu Asn Asn Ile Arg Lys Thr Ser Leu Phe Pro Arg Asp Pro Gln
223     130                 135                 140
225 Arg Leu Val Pro
226 145
228 <210> SEQ ID NO: 5
229 <211> LENGTH: 1109
230 <212> TYPE: DNA
231 <213> ORGANISM: Glycine max
233 <400> SEQUENCE: 5
234 gcacgaggtc atcagagaga atggcttcac cgttcaatgc ttggtgcagg cgcaggccga    60
235 tacggtgagc ccgcagatgg tgaagttcgc cgctgcactc agccgcgagt ccatcgtcga   120
236 tgtcgaaggc gttgtttcga tcccctccgc tcccatcaaa ggcgccacac aacaggtgga   180
237 aattcaagtg aggaagttgt attgtgtcag tagggctgta cctactctgc ctattaatct   240
238 tgaggatgct gctcgaagtg aagttgaaat cgagacggct cttcaggctg gtgagcaact   300
239 tgttcgtgtt aatcaggata cacgtctgaa ctttagggtg cttgatgtgc gaacgccagc   360
240 taatcaaggg attttccgca ttcagtctca agttggaaat gcgtttagac aattcttatt   420
241 atctgaaggt ttttgtgaaa tccacactcc aaagttgata gctggatcta gtgagggagg   480
242 agctgctgtt tttagactgg actacaaagg tcaacctgca tgcctggccc agtcacctca   540
243 gcttcacaag caaatgtcta tttgtggaga ttttggccgt gtttttgaga ttggtcctgt   600
244 gtttagagca gaagattcct acactcacag gcatctgtgt gagtttacag gtcttgatgt   660
245 tgaaatggag attaagaagc attactttga ggttatggat atagtcgata gattgtttgt   720
246 cgcaatgttt gacagtttga accagaattg taagaaggat ctggaagctg tcgggtctca   780
247 gtatccattt gaacctttga agtatctgcg gacgacacta cggcttacat atgaagaagg   840
248 gattcagatg ctcaaggatg ttggagtaga aattgaacct tatggtgact tgaatactga   900
249 agcggaaagg aaattgggtc agctagtctc agagaaatat ggcacagagt tctatatcct   960
250 tcaccggtac cctttggctg taaggccatt ctatacaatg ccttgctacg acaatcctgc  1020
251 atacagcaac tcgtttgatg tctttattcg aggtgaggag ataatttcag gagctcagcg  1080
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Input Set : **A:\BB-1191 Seq List.txt**
Output Set: **N:\CRF3\03112002\I846589A.raw**

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252 tgttcatgtg ccagaatttt tggaacaag                              1109
254 <210> SEQ ID NO: 6
255 <211> LENGTH: 369
256 <212> TYPE: PRT
257 <213> ORGANISM: Glycine max
259 <400> SEQUENCE: 6
260 His Glu Val Ile Arg Glu Asn Gly Phe Thr Val Gln Cys Leu Val Gln
261   1               5                  10                  15
263 Ala Gln Ala Asp Thr Val Ser Pro Gln Met Val Lys Phe Ala Ala Ala
264              20                  25                  30
266 Leu Ser Arg Glu Ser Ile Val Asp Val Glu Gly Val Val Ser Ile Pro
267          35                  40                  45
269 Ser Ala Pro Ile Lys Gly Ala Thr Gln Gln Val Glu Ile Gln Val Arg
270      50                  55                  60
272 Lys Leu Tyr Cys Val Ser Arg Ala Val Pro Thr Leu Pro Ile Asn Leu
273  65                  70                  75                  80
275 Glu Asp Ala Ala Arg Ser Glu Val Glu Ile Glu Thr Ala Leu Gln Ala
276                  85                  90                  95
278 Gly Glu Gln Leu Val Arg Val Asn Gln Asp Thr Arg Leu Asn Phe Arg
279              100                 105                 110
281 Val Leu Asp Val Arg Thr Pro Ala Asn Gln Gly Ile Phe Arg Ile Gln
282          115                 120                 125
284 Ser Gln Val Gly Asn Ala Phe Arg Gln Phe Leu Leu Ser Glu Gly Phe
285      130                 135                 140
287 Cys Glu Ile His Thr Pro Lys Leu Ile Ala Gly Ser Ser Glu Gly Gly
288 145                 150                 155                 160
290 Ala Ala Val Phe Arg Leu Asp Tyr Lys Gly Gln Pro Ala Cys Leu Ala
291              165                 170                 175
293 Gln Ser Pro Gln Leu His Lys Gln Met Ser Ile Cys Gly Asp Phe Gly
294              180                 185                 190
296 Arg Val Phe Glu Ile Gly Pro Val Phe Arg Ala Glu Asp Ser Tyr Thr
297          195                 200                 205
299 His Arg His Leu Cys Glu Phe Thr Gly Leu Asp Val Glu Met Glu Ile
300      210                 215                 220
302 Lys Lys His Tyr Phe Glu Val Met Asp Ile Val Asp Arg Leu Phe Val
303 225                 230                 235                 240
305 Ala Met Phe Asp Ser Leu Asn Gln Asn Cys Lys Lys Asp Leu Glu Ala
306              245                 250                 255
308 Val Gly Ser Gln Tyr Pro Phe Glu Pro Leu Lys Tyr Leu Arg Thr Thr
309              260                 265                 270
311 Leu Arg Leu Thr Tyr Glu Glu Gly Ile Gln Met Leu Lys Asp Val Gly
312          275                 280                 285
314 Val Glu Ile Glu Pro Tyr Gly Asp Leu Asn Thr Glu Ala Glu Arg Lys
315      290                 295                 300
317 Leu Gly Gln Leu Val Ser Glu Lys Tyr Gly Thr Glu Phe Tyr Ile Leu
318 305                 310                 315                 320
320 His Arg Tyr Pro Leu Ala Val Arg Pro Phe Tyr Thr Met Pro Cys Tyr
321              325                 330                 335
323 Asp Asn Pro Ala Tyr Ser Asn Ser Phe Asp Val Phe Ile Arg Gly Glu
```

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/846,589A**

DATE: 03/11/2002
TIME: 09:44:17

Input Set : **A:\BB-1191 Seq List.txt**
Output Set: **N:\CRF3\03112002\I846589A.raw**

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:15 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD